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1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/721,212

DATE: 09/22/2003

TIME: 10:43:44

Input Set : A:\A-451K REV 091003-54.txt

Output Set: N:\CRF4\09222003\I721212.raw

3 <110> APPLICANT: BOYLE, WILLIAM
 5 <120> TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS
 7 <130> FILE REFERENCE: A-451K REV 09-10-03 54SEQ
 9 <140> CURRENT APPLICATION NUMBER: US 09/721,212
 10 <141> CURRENT FILING DATE: 2000-11-21
 12 <150> PRIOR APPLICATION NUMBER: US 09/052,521
 13 <151> PRIOR FILING DATE: 1998-03-30
 15 <150> PRIOR APPLICATION NUMBER: US 08/880,855
 16 <151> PRIOR FILING DATE: 1997-06-23
 18 <150> PRIOR APPLICATION NUMBER: US 08/842,842
 19 <151> PRIOR FILING DATE: 1997-04-16
 21 <160> NUMBER OF SEQ ID NOS: 54
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 2295
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Mus musculus
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (158)..(1105)
 33 <223> OTHER INFORMATION:

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 41 tcgcggagca gggcgcccga actccggggcg ccgcgcc atg cgc cgg gcc agc cga 175
 42 Met Arg Arg Ala Ser Arg
 43 1 5
 45 gac tac ggc aag tac ctg cgc agc tcg gag gag atg ggc agc ggc ccc 223
 46 Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro
 47 10 15 20
 49 ggc gtc cca cac gag ggt ccg ctg cac ccc gcg cct tct gca ccg gct 271
 50 Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala
 51 25 30 35
 53 ccg gcg ccg cca ccc gcc gcc tcc cgc tcc atg ttc ctg gcc ctc ctg 319
 54 Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu
 55 40 45 50
 57 ggg ctg gga ctg ggc cag gtg gtc tgc agc atc gct ctg ttc ctg tac 367
 58 Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr
 59 55 60 65 70
 61 ttt cga gcg cag atg gat cct aac aga ata tca gaa gac agc act cac 415
 62 Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His
 63 75 80 85
 65 tgc ttt tat aga atc ctg aga ctc cat gaa aac gca ggt ttg cag gac 463

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69	tcg	act	ctg	gag	agt	gaa	gac	aca	cta	cct	gac	tcc	tgc	agg	agg	atg	511
70	Ser	Thr	Leu	Glu	Ser	Glu	Asp	Thr	Leu	Pro	Asp	Ser	Cys	Arg	Arg	Met	
71			105					110					115				
73	aaa	caa	gcc	ttt	cag	ggg	gcc	gtg	cag	aag	gaa	ctg	caa	cac	att	gtg	559
74	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	Lys	Glu	Leu	Gln	His	Ile	Val	
75		120					125					130					
77	ggg	cca	cag	cgc	ttc	tca	gga	gct	cca	gct	atg	atg	gaa	ggc	tca	tgg	607
78	Gly	Pro	Gln	Arg	Phe	Ser	Gly	Ala	Pro	Ala	Met	Met	Glu	Gly	Ser	Trp	
79	135					140					145				150		
81	ttg	gat	gtg	gcc	cag	cga	ggc	aag	cct	gag	gcc	cag	cca	ttt	gca	cac	655
82	Leu	Asp	Val	Ala	Gln	Arg	Gly	Lys	Pro	Glu	Ala	Gln	Pro	Phe	Ala	His	
83				155					160					165			
85	ctc	acc	atc	aat	gct	gcc	agc	atc	cca	tcg	ggt	tcc	cat	aaa	gtc	act	703
86	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	Thr	
87			170					175					180				
89	ctg	tcc	tct	tgg	tac	cac	gat	cga	ggc	tgg	gcc	aag	atc	tct	aac	atg	751
90	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Asn	Met	
91		185					190					195					
93	acg	tta	agc	aac	gga	aaa	cta	agg	gtt	aac	caa	gat	ggc	ttc	tat	tac	799
94	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	
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97	ctg	tac	gcc	aac	att	tgc	ttt	cgg	cat	cat	gaa	aca	tcg	gga	agc	gta	847
98	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	His	Glu	Thr	Ser	Gly	Ser	Val	
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101	cct	aca	gac	tat	ctt	cag	ctg	atg	gtg	tat	gtc	gtt	aaa	acc	agc	atc	895
102	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	Tyr	Val	Val	Lys	Thr	Ser	Ile	
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105	aaa	atc	cca	agt	tct	cat	aac	ctg	atg	aaa	gga	ggg	agc	acg	aaa	aac	943
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110	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	Tyr	Ser	Ile	Asn	Val	Gly	Gly	
111		265				270					275						
113	ttt	ttc	aag	ctc	cga	gct	ggt	gaa	gaa	att	agc	att	cag	gtg	tcc	aac	1039
114	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	Ile	Ser	Ile	Gln	Val	Ser	Asn	
115		280				285					290						
117	cct	tcc	ctg	ctg	gat	ccg	gat	caa	gat	gcg	acg	tac	ttt	ggg	gct	ttc	1087
118	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	Ala	Thr	Tyr	Phe	Gly	Ala	Phe	
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121	aaa	gtt	cag	gac	ata	gac	tgagactcat	ttcgtggaac	attagcatgg								1135
122	Lys	Val	Gln	Asp	Ile	Asp											
123				315													
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127	actaagagac	atggccacg	gtgtatgaaa	ctcacagccc	tctctcttga	gcctgtacag											1255
129	gttgtgtata	tgtaaagtcc	ataggtgatg	ttagattcat	ggtgattaca	caacggtttt											1315
131	acaattttgt	aatgatttcc	tagaattgaa	ccagattggg	agaggtattc	cgatgcttat											1375
133	gaaaaactta	cacgtgagct	atggaagggg	gtcacagtct	ctgggtctaa	cccctggaca											1435

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139 tttctaataa ggagagaaaa atatatgtat ttttatataa tgtctaaagt tatatttcag 1615
141 gtgtaatggt ttctgtgcaa agttttgtaa attatatattg tgctatagta tttgattcaa 1675
143 aatatttaaa aatgtctcac tgttgacata tttaatgttt taaatgtaca gatgtattta 1735
145 actggtgcac ttgttaattc cctgaaggt actcgtagct aagggggcag aatactgttt 1795
147 ctggtgacca catgtagttt atttctttat tctttttaac ttaatagagt cttcagactt 1855
149 gtcaaaacta tgcaagcaaa ataaataaat aaaaataaaa tgaatacctt gaataataag 1915
151 taggatgttg gtcaccaggt gcctttcaaa tttagaagct aattgacttt aggagctgac 1975
153 atagccaaaa aggatacata ataggctact gaaatctgtc aggagtattt atgcaattat 2035
155 tgaacagggtg tcttttttta caagagctac aaattgtaaa ttttgtttct tttttttccc 2095
157 atagaaaatg tactatagtt tatcagccaa aaaacaatcc actttttaat ttagtgaaag 2155
159 ttattttatt atactgtaca ataaaagcat tgtctctgaa tgtaattttt ttggtacaaa 2215
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168 <212> TYPE: PRT
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178 20 25 30
181 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
182 35 40 45
185 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
186 50 55 60
189 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
190 65 70 75 80
193 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
194 85 90 95
197 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
198 100 105 110
201 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
202 115 120 125
205 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
206 130 135 140
209 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
210 145 150 155 160
213 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
214 165 170 175
217 Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
218 180 185 190
221 Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
222 195 200 205
225 Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
226 210 215 220
229 Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr

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230 225          230          235          240
233 Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
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237 Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
238          260          265          270
241 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
242          275          280          285
245 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
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249 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
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261 <223> OTHER INFORMATION:

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269 cgcagacaag aaggggaggg agcgggagag ggaggagagc tccgaagcga gagggccgag      180
271 cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tcg      229
272 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser
273 1          5          10          15
275 gag gag atg ggc ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac      277
276 Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His
277          20          25          30
279 gcc ccg ccg ccg cct gcg ccg cac cag ccc ccc gcc gcc tcc cgc tcc      325
280 Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser
281          35          40          45
283 atg ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc      373
284 Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
285          50          55          60
287 gtc gcc ctg ttc ttc tat ttc aga gcg cag atg gat cct aat aga ata      421
288 Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
289          65          70          75
291 tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa      469
292 Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu
293 80          85          90          95
295 aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta      517
296 Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu
297          100          105          110
299 ata cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg      565
300 Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val
301          115          120          125
303 caa aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag      613
304 Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu

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309          145          150          155
311 ctt gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc      709
312 Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile
313 160          165          170          175
315 cca tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg      757
316 Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg
317          180          185          190
319 ggt tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata      805
320 Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile
321          195          200          205
323 gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga      853
324 Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg
325          210          215          220
327 cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg      901
328 His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met
329          225          230          235
331 gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg      949
332 Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu
333 240          245          250          255
335 atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat      997
336 Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His
337          260          265          270
339 ttt tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag      1045
340 Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu
341          275          280          285
343 gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag      1093
344 Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
345          290          295          300
347 gat gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat      1135
348 Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
349          305          310          315
351 tgagccccag tttttggagt gttatgtatt tcttgatgt ttggaaacat tttttaaaac      1195
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371 acagacatat ttaactggtg cactttgtaa attccctggg gaaaacttgc agctaaggag      1795
373 gggaaaaaaa tgttgtttcc taatatcaaa tgcagtatat ttcttcgttc tttttaagtt      1855
375 aatagatttt ttcagacttg tcaagcctgt gcaaaaaaat taaaatggat gccttgaata      1915
377 ataagcagga tgttggccac caggtgcctt tcaaatttag aaactaattg actttagaaa      1975
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L:264 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:261
L:967 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:42,Line#:964